UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/553,436	03/21/2006	Robert A. Macina	DEX0477US.NP	6995

32800 7590 09/18/2006

LICATA & TYRRELL P.C.
66 E. MAIN STREET
MARLTON, NJ 08053

EXAMINER	
ZHOU, SHUBO	
ART UNIT	**PAPER NUMBER**
1631	

DATE MAILED: 09/18/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/553,436	MACINA ET AL.	
	Examiner	Art Unit	
	Shubo (Joe) Zhou	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *14 July 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-18* is/are pending in the application.

4a) Of the above claim(s) *7,11-15 and 17* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-6,8-10,16 and 18* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *11 October 2005* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *10/11/05,8/29/06,9/7/06*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☒ Other: *see continuation sheet*.

Continuation of Attachments 6):

1. Sequence alignment between SEQ ID NO:36 and M15041
2. Sequence alignment between SEQ ID NO:36 and SEQ ID NO:52

DETAILED ACTION

Election/Amendments

1. Applicants' election, with traverse, of Group I, drawn to polynucleotides (claims 1-6, 8-10, 16 in part and 18 in part) and SEQ ID NO:36 in the response filed 7/14/06 is acknowledged. The traversal is on the ground(s) that there would be no serious search burden to examine all the groups together, and that requirement of election of a single sequence is improper. This is not found persuasive because, firstly, reasons that there would be a serious search burden if groups I-IV were examined were set forth in the previous Office action on pages 3-7. Applicants do not argue against those reasons. With regard to the single sequence election requirement, as also set forth in the previous Office action on page 7, that "the multitude of sequence submissions for examination has resulted in an undue search burden if more than one nucleic acid sequence is elected, thus making the previous waiver for up to 10 elected nucleic acid sequences effectively impossible to reasonably implement."

The requirement is still deemed proper and is therefore made FINAL.

Accordingly, claims 1-18 are currently pending, but only claims 1-6, 8-10, 16 in part and 18 in part are under examination. Claims 16 and 18 are examined to the extent of the elected invention, i.e. nucleic acids.

Claims 7, 11-15 and 17 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected inventions, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on 7/14/06.

The preliminary amendment to the specification filed on 10/11/05 is also acknowledged and entered.

Sequence Rules Compliance

2. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). Such sequences are present in Figures 1-3 and 5. However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 because there sequences are not followed by a sequence identifier ("SEQ ID NO:X"). Applicants are reminded that it is required that SEQ ID Nos be amended into the specification at each sequence, and that when a sequence is presented in a drawing regardless of the format or the manner of presentation of that sequence in the drawing, the sequence must still be included in the Sequence Listing and the sequence identifier ("SEQ ID NO:X") must be used, either in the drawing or in the Brief Description of the Drawings.

Applicants are given the same response time regarding this failure to comply as that set forth to respond to this office action. Failure to comply with these requirements may result in ABANDONMENT of the application under 37 CFR 1.821(g).

Information Disclosure Statement

3. The Information Disclosure Statements filed 10/11/05, 8/29/06, and 9/7/06 have been entered and references disclosed therein have been considered. Initialed copies of the form PTO-1449 are enclosed with this action.

Drawings

4. The drawings filed 10/11/05 are objected to because of the following:

37 CFR 1.84(u) states:

Partial views intended to form one complete view, on one or several sheets, must be identified by the same number followed by a capital letter. View numbers must be preceded by the abbreviation "Fig."

In the instant application, sheets 1-9 are partial views of a sequence alignment, sheets 10-12 are partial views of a sequence alignment, sheets 13-18 are partial views of a sequence alignment, and sheets 20-21 are partial views of another sequence alignment. These partial views are not identified as required by 37 CFR 1.84 as set forth above. It is suggested that the partial views be numbered, e.g. as Fig. 1A, Fig. 1B, etc.

Corrected drawing sheets in compliance with 37 CFR 1.121(d) are required in reply to the Office action to avoid abandonment of the application. Any amended replacement drawing sheet should include all of the figures appearing on the immediate prior version of the sheet, even if only one figure is being amended. The figure or figure number of an amended drawing should not be labeled as "amended." If a drawing figure is to be canceled, the appropriate figure must be removed from the replacement sheet, and where necessary, the remaining figures must be renumbered and appropriate changes made to the brief description of the several views of the drawings for consistency. Additional replacement sheets may be necessary to show the renumbering of the remaining figures. Each drawing sheet submitted after the filing date of an application must be labeled in the top margin as either "Replacement Sheet" or "New Sheet" pursuant to 37 CFR 1.121(d). If the changes are not accepted by the examiner, the applicant will be notified and informed of any required corrective action in the next Office action. The objection to the drawings will not be held in abeyance.

Specification

5. The specification is objected to because of the following:

The title of the invention is not descriptive. The elected invention is drawn to an isolated nucleic acid. The current title, however, is directed to compositions, splice variants and methods relating to cancer specific genes and proteins. A new title is required that is clearly indicative of the invention to which the elected claims are directed.

It appears that trademark is used in this application, such as PLATINOL on page 24. It should be capitalized wherever it appears and be accompanied by the generic terminology. Although the use of trademarks is permissible in patent applications, the proprietary nature of the marks should be respected and every effort made to prevent their use in any manner which might adversely affect their validity as trademarks.

The disclosure is objected to also because it contains an embedded hyperlink and/or other form or browser-executable code. Such code is present in the specification at page 24 and elsewhere. Applicants are required to delete all the embedded hyperlinks and/or other forms of browser-executable code. See MPEP ' 608.01.

There are many tables disclosed in the specification, e.g. the tables on pages 37, 153-157, 158-249. Not all tables are numbered, and confusingly, the table that is labeled as Table 1 is not the first table disclosed in the specification. See page 255.

It seems that the word "form" before the phrase "the same patient" on page 394, line 6, should be "from."

Appropriate correction is required.

Claim Rejections-35 USC § 101 and § 112

6. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

7. Claims 1-6, 8-10, 16 and 18 are rejected under 35 U.S.C. 101 because the claimed invention lacks patentable utility due to its not being supported by a specific, substantial, and credible utility or, in the alternative, a well-established utility.

Claims 1-6, 8-10, 16 and 18 are drawn to isolated nucleic acid molecules comprising the sequence of SEQ ID NO:36 or a sequence that encodes the amino acid sequence of SEQ ID NO:194, which is encoded by SEQ ID NO:36.

The specification discloses that the sequence of SEQ ID NO:36 is also referred to as DEX0477_020.nt.2 (see page 154), which is, in turn, referred to also as Cln224v1 (see page 392).

The claimed nucleic acid molecule is not supported by a specific, substantial and credible asserted utility.

The specification asserts that Cln224v1 is "useful as a diagnostic marker and/or therapeutic target for cancers of the gastrointestinal tract." See page 394, lines 7-10.

Consideration of the expression of Cln224v1 in different cancer tissues disclosed in the specification reveals that this is not a substantial and credible utility.

The specification on pages 394-395 discloses that 40% of the colon cancer samples have an over-expression of Cln224v1 as compared to normal tissues or normal adjacent tissues, but also 44% of lung cancer samples and 22% of breast cancer tissues have an over-expression of Cln224v1 as compared to normal tissues or normal adjacent tissues. Furthermore, 50% of the colon cancer samples have a down-expression of Cln224v1 as compared to normal tissues or

normal adjacent tissues, and 33 % of lung cancer samples have a down-expression of Cln224v1 as compared to normal tissues or normal adjacent tissues. No statistical analyses are given to indicate any statistical significance of the data. For a nucleic acid molecules that is over-expressed in some colon cancer samples, in some lung cancer samples and some breast cancer samples, and at the same time, it is also down-expressed in certain colon cancer samples and in certain lung cancer samples, one skilled in the art would have reasonable doubt that it would be "useful as a diagnostic marker and/or therapeutic target for cancers of the gastrointestinal tract." Further research is apparently needed to determine whether such a molecule can be used as such a marker. The apparent need for such research indicates that the nucleic acid molecule is not disclosed as to a currently available or substantial utility.

Recently, in *In re Fisher,* a case analogous to the present application, the court, following an analysis of Nelson, 626 F.2d at 856, with regard to substantial utility, states that "it thus is clear that an application must show that an invention is useful to the public as disclosed in its current form, not that it may prove useful at some future date after further research." *In re Fisher*, 76 USPQ2d 1225 1230 (CAFC 2005). In the instant case, the application does not show that the claimed polynucleotide is useful to the public as disclosed in its current form, but that it may prove useful at some future date after further research.

Further, neither the specification as filed nor any art of record discloses or suggests any property or activity for the nucleic acid comprising SEQ ID NO:36 or the polypeptide encoded thereby such that another non-asserted utility would be well established for the nucleic acid or its encoded polypeptide.

8. The following is a quotation of the **first** paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

9. Claims 1-6, 8-10, 16 and 18 are rejected under 35 U.S.C. 112, first paragraph.

Specifically, since the claimed invention lacks a patentable utility due to its not being supported by a specific, substantial, and credible utility or, in the alternative, a well-established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

10. Claims 16 and 18 are also rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claims contain subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

In *In re Wands* (8 USPQ2d 1400 (CAFC 1988)), the CAFC considered the issue of enablement in molecular biology. The CAFC summarized eight factors to be considered in a determination of "undue experimentation". These factors include: (a) the quantity of experimentation; (b) the amount of guidance presented; (c) the presence or absence of working examples; (d) the nature of the invention; (e) the state of the prior art; (f) the predictability of the prior art; (g) the breadth of the claims; and (h) the relative skill in the art. The factors are analyzed for the instant case as follows:

In the instant case, the amount of experimentation required by the skilled artisan in order to practice of using the claimed nucleic acid for detecting a risk or presence of cancer in a patient

or as a vaccine would require an unpredictable amount of experimentation for the following reasons:

The claims are drawn to a kit comprising the claimed nucleic acid for detecting a risk or presence of cancer in a patient (claim 16) or a vaccine comprising the claimed nucleic acid. As set forth above, the specification on pages 394-395 discloses that 40% of the colon cancer samples have an over-expression of Cln224v1 as compared to normal tissues or normal adjacent tissues, but also 44% of lung cancer samples and 22% of breast cancer tissues have an over-expression of Cln224v1 as compared to normal tissues or normal adjacent tissues. Furthermore, 50% of the colon cancer samples have a down-expression of Cln224v1 as compared to normal tissues or normal adjacent tissues, and 33 % of lung cancer samples have a down-expression of Cln224v1 as compared to normal tissues or normal adjacent tissues. No statistical analyses are given to indicate any statistical significance of the data. For a nucleic acid molecules that is over-expressed in some colon cancer samples, in some lung cancer samples and some breast cancer samples, and at the same time, it is also down-expressed in certain colon cancer samples and in certain lung cancer samples, one skilled in the art would not know how to use it to detect the risk or presence of a cancer in a patient or use it as a vaccine. The specification does not provide guidance, nor does it provide any working example, as to how to use such a nucleic acid molecule to detect the risk or presence of a cancer in a patient or use it as a vaccine.

The nature of the invention, i.e. a kit comprising a nucleic acid molecule for use to detect the risk or presence of a cancer in a patient or as a vaccine, is complex. The prior art does not teach or fairly suggest such a kit or vaccine. The skilled practitioner would first turn to the instant specification for guidance in practice of using the kit comprising the nucleic acid molecule comprising the sequence of SEQ ID NO:36 to detect the risk or presence of a cancer in a patient or use it as a vaccine. However, the specification does not provide sufficient guidance

or working example of practicing the invention. As such, the skilled practitioner would turn to the prior art for such guidance. However, the prior art does not teach such a kit or vaccine. Finally, said practitioner would have to turn to trial and error experimentation for practicing using the claimed nucleic acid for detecting the risk or presence of a cancer in a patient or use it as a vaccine without adequate guidance from the specification or the prior art. Therefore, undue experimentation becomes the burden of the practitioner.

11. Claims 1-6, 8-10, 16 and 18 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are rejected mostly for the same reasons as those set forth in the "Revised Interim Written Description Guidelines Training Material" for similar claim limitations. The training material is available on the US PTO's website: http://www.uspto.gov/web/patents/guides.htm, and its relevant sections are attached to this Office action. Please especially see Examples 6, 9, 10, 11, and 13.

The claims are drawn to a genus of nucleic acid molecules including any nucleic acid molecule that selectively hybridizes to the nucleic acid of SEQ ID NO:36 or any nucleic acid molecules that encode the polypeptide of SEQ ID NO:194, which is also encoded by SEQ ID NO:36. Since the claims do not specify any stringency conditions for the hybridizations, and do not contain functional limitations, the claims are broad and read on virtually any nucleic acids

because almost any polynucleotides can hybridize to the a molecule comprising SEQ ID NO:36 under certain hybridization conditions and the hybridization is selective because it would not hybridize to other molecules such as proteins as the specification does not explicitly defines the metes and bounds of the phrase "selectively hybridize." Clearly, there is substantial variability among the species encompassed by the scope of the claims because the genus encompasses a variety of species with different structures and distinct functions.

A description of a genus may be achieved by means of a recitation of a representative number of species, falling within the scope of the genus, or by means of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus. Regents of the University of California v. Eli Lilly & Co., 119 F3d 1559, 1569, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). In the instant case, the specification discloses only a species: the nucleotide sequence of SEQ ID NO:36, but, as set forth above, the lack of stringency of hybridization conditions and the lack of functional limitation would be expected to yield structurally unrelated nucleic acid molecules. Thus, the single disclosed species is not representative of the genus because there is no structural attribute or feature that is common to the members of the genus.

Therefore, one skilled in the relevant art would have reasonable doubt that the inventor(s), at the time the application was filed, had possession of the claimed invention.

12. The following is a quotation of the **second** paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

13. Claims 2-6, 8-10, 16 and 18 are rejected under 35 U.S.C. 112 , second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 2-6, 8-10, 16 and 18 all recite the phrase "the nucleic acid molecule according to claim 1, wherein the nucleic acid molecule." Claim 1 refers to multiple different nucleic acid molecules: the nucleic acid molecule of (a), of (b), of (c), of (d), and the nucleic acid molecule comprising the molecule of (a), (b), (c), or (d). Thus, it is not clear as to what nucleic acid molecule is referred to in claims 2-6, 8-10, 16 and 18 by "the nucleic acid molecule according to claim 1."

Clarification of the metes and bounds of the claims is requested.

Claim Rejections-35 USC § 102

14. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

15. Claims 1-2, 4-6, 8-10, and 16 are rejected under 35 U.S.C. § 102(b) as being anticipated by Oikawa et al. (Biochemical and Biophysical Research Communications, Vol. 142, pages 511-518).

The claims are drawn to any nucleic acid molecules that selectively hybridize to the nucleic acid of SEQ ID NO:36.

Oikawa et al. disclose a nucleic acid molecule, referred to as CEA, comprising a sequence that is about 80% identical to the sequence of SEQ ID NO:36. See the attached sequence alignment between SEQ ID NO:36 and the sequence of GenBank accession number

M15041, which is the same sequence as that disclosed by Oikawa et al. See the text portion of the sequence alignment. Given that the two sequences share such a relatively high sequence identity and that the claims do not specify any hybridization conditions, it would be readily apparent to one skilled in the art that the two sequences would hybridize to each under certain, e.g. low to medium conditions, and the hybridization would be selective because they would not hybridize to other molecules such as proteins.

As to claim 2, Oikawa et al. disclose a cDNA molecule comprising the sequence.

As to claims 4-6, given that Oikawa et al. disclose that the cDNA was obtained from RNA of human colon tissues (see pages 512-513), it is apparent that Oikawa et al. also disclose an RNA molecule that hybridizes with the nucleic acid comprising SEQ ID NO:36, and the nucleic acid molecules are from human, which is a mammal.

As to claims 8-9, Oikawa et al. disclose that the cDNA is in the vector lambda gt11 and in E. coli cells.

As to claim 10, Oikawa et al. disclose that the cDNA clone from the cDNA library is done by immunoscreening assays with a rabbit anti-CEA antibody. Given that it would be well known that the lambda gt11 vector is an expression vector comprising control sequences allowing the expression and translation of the insert sequence, and that the immunoscreening assay is an assay wherein the insert is allowed to be expressed and polypeptide is produced in the host cells before the binding assay with the antibody, it is apparent that Oikawa et al. disclose a method for producing the polypeptide encoded by CEA.

As to claim 16, given that the CEA cDNA is isolated by Oikawa et al. in a laboratory, it must have been contained in a container. Such a container having therein the cDNA is interpreted as being a kit.

16. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (f) he did not himself invent the subject matter sought to be patented.

17. Claims 1-6, 8-10, 16 and 18 are rejected under 35 U.S.C. 102(f) because the applicant did not invent the claimed subject matter.

For the reasons discussed below in the section of double patenting rejection, it is apparent that copending Application No. 10/558861 contains claimed subject matter in claims that is not patentably distinct from instant claims 1-6, 8-10, 16 and 18. Because the inventive entity of copending Application 10/558861 is different from the instant application, a rejection is appropriate under 35 U.S.C. 102(f). This rejection could be overcome by amendment of the appropriate claims so that the claims are patentably distinct, or by filing a declaration stating the inventive entity for the commonly claimed subject matter is identical.

Provisional Double Patenting

18. The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970);and, *In re Thorington,* 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground

provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

19. Claims 1-6, 8-10, 16 and 18 are provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 1-6, 8-10, 16 and 18 of US copending Application No. 10/558861.

An obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but an examined application claim is not patentably distinct from the reference claims because the examined claim is either anticipated by, or would have been obvious over, the reference claims. See, e.g., *In re Berg*, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985). Although the conflicting claims are not identical, they are not patentably distinct from each other.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

Claims 1-6, 8-10, 16 and 18 of the instant application are drawn to nucleic acid molecules comprising the sequence of SEQ ID NO:36 or any nucleic acid that encodes the polypeptide of SEQ ID N):194, which is encoded by SEQ ID NO:36, or any nucleic acids that hybridize selectively with any of the above.

At least for one embodiment, 1-6, 8-10, 16 and 18 of US copending Application No. 10/558861 are drawn to nucleic acid molecules comprising the sequence of SEQ ID NO:52 or any nucleic acid that hybridizes selectively with the sequence of SEQ ID NO:52. Sequence comparison performed by the Office shows that the sequence of SEQ ID NO:52 of the copending application is identical to the SEQ ID NO:36 of the instant application. Thus, claims 1-6, 8-10, 16 and 18 of the instant application are anticipated by claims 1-6, 8-10, 16 and 18 of the copending US application, respectively.

Conclusion

20. No claim is allowed.

21. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Shubo (Joe) Zhou, whose telephone number is 571-272-0724. The examiner can normally be reached Monday-Friday from 8 A.M. to 4 P.M. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Andrew Wang, can be reached on 571-272-0811. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of

the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public. For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

Shubo (Joe) Zhou, Ph.D. 9/8/06

Patent Examiner

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: August 9, 2006, 13:58:38 ; Search time 3020 Seconds
(without alignments)
7787.217 Million cell updates/sec

Title: US-10-553-436-36
Perfect score: 3373
Sequence: 1 ggaagagactcagggcagag.....tccagcctgggagacaaagt 3373

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3373	100.0	3373	13	ADT50732	Adt50732 Cancer re
2	3373	100.0	3373	14	ADY30457	Ady30457 Human spl
3	3261.4	96.7	3470	14	AEC79249	Aec79249 Human CEA
4	3174	94.1	3462	13	ADT50731	Adt50731 Cancer re
5	2834	84.0	3892	14	ADY30456	Ady30456 Human spl
6	2824.4	83.7	3897	14	AEC79247	Aec79247 Human CEA
7	2824.4	83.7	3897	15	AEE80154	Aee80154 Human ova
8	2780.8	82.4	3036	12	ADO49152	Ado49152 Human car
9	2696.4	79.9	4217	14	AEC79250	Aec79250 Human CEA
10	2685.4	79.6	2975	6	ABQ82535	Abq82535 Human CEA
11	2680	79.5	2928	2	AAT75431	Aat75431 Human car
12	2669.2	79.1	2974	6	ABL64746	Abl64746 Lung canc
13	2669.2	79.1	2974	6	ABN95819	Abn95819 Gene #231
14	2669.2	79.1	2974	8	ABX76144	Abx76144 Lung canc
15	2669.2	79.1	2974	8	ABX76396	Abx76396 Lung canc
16	2669.2	79.1	2974	8	ADA84058	Ada84058 Human CEA
17	2669.2	79.1	2974	8	ABQ83855	Abq83855 Human CEA
18	2669.2	79.1	2974	9	ACF35963	Acf35963 Human car
19	2669.2	79.1	2974	10	ADC09592	Adc09592 CEA cDNA
20	2669.2	79.1	2974	10	ADD25525	Add25525 Binding d
21	2669.2	79.1	2974	11	ADN39013	Adn39013 Cancer/an
22	2669.2	79.1	2974	12	ADM32425	Adm32425 Human can
23	2669.2	79.1	2974	12	ADM72830	Adm72830 Human CEA
24	2669.2	79.1	2974	12	ADO28644	Ado28644 Human CEA
25	2669.2	79.1	2974	12	ADQ29579	Adq29579 Human col
26	2669.2	79.1	2974	13	ADU06134	Adu06134 Novel bro
27	2669.2	79.1	2974	14	ADW77716	Adw77716 Human car
28	2669.2	79.1	2974	14	AEB22713	Aeb22713 Human col
29	2669.2	79.1	2974	14	AEB29684	Aeb29684 Human car
30	2669.2	79.1	2974	15	AEF68538	Aef68538 Human car
31	2669.2	79.1	2974	15	AEF69891	Aef69891 Colorecta
32	2666.8	79.1	2969	14	ADV73190	Adv73190 Human col
33	2666.8	79.1	2969	14	ADV73186	Adv73186 Human col
34	2659.2	78.8	2928	1	AAN81611	Aan81611 Carcinoem
35	2551	75.6	2839	1	AAN92780	Aan92780 cDNA sequ
36	2551	75.6	2839	2	AAQ54352	Aaq54352 Carcinoem
37	2551	75.6	2839	2	AAT46062	Aat46062 Carcinoem
38	2544.6	75.4	2839	2	AAV70153	Aav70153 CEA prote
39	2539.8	75.3	2839	1	AAN81584	Aan81584 1LV7 cDNA
40	2261.8	67.1	2728	5	ADL62676	Adl62676 Human ova
41	2247.4	66.6	2625	13	ACN41292	Acn41292 Human dia
42	2156.4	63.9	2963	14	AEC79251	Aec79251 Human CEA
43	2141.2	63.5	3347	15	AEE80155	Aee80155 Human ova
44	2139.4	63.4	2259	12	ADQ86883	Adq86883 Human tum
45	2129.2	63.1	3346	14	AEC79248	Aec79248 Human CEA
46	2121.4	62.9	2389	4	AAF61687	Aaf61687 Human car
47	2115.8	62.7	2220	2	AAT33302	Aat33302 Carcinoem
48	2034.6	60.3	6211	14	AEF80401	Aef80401 Carcinoem
49	2028.2	60.1	2263	15	AEF70034	Aef70034 Human CEA
50	2027	60.1	2109	13	ADU73923	Adu73923 Human car
51	2027	60.1	2167	14	AEB96459	Aeb96459 Lysosome-
52	2027	60.1	2349	2	AAQ67869	Aaq67869 H6/CEA ex
53	2027	60.1	2349	2	AAZ08470	Aaz08470 H6/CEA ex
54	2027	60.1	2349	13	ADR21837	Adr21837 Recombina
55	2027	60.1	2434	2	AAQ67868	Aaq67868 H6/CEA ex
56	2027	60.1	2434	2	AAZ08469	Aaz08469 H6/CEA ex
57	2027	60.1	2434	13	ADR21836	Adr21836 Recombina
58	2026	60.1	2031	2	AAQ71567	Aaq71567 Carcinoem
59	2026	60.1	2037	14	AEB96455	Aeb96455 Human CEA
60	2026	60.1	2355	14	AEB96442	Aeb96442 CEA-LTB f
61	2026	60.1	2766	14	AEB96440	Aeb96440 CEA-LTA f
62	2026	60.1	2857	14	AEB96482	Aeb96482 hCEAopt-D
63	2026	60.1	3426	14	AEB96457	Aeb96457 Tetanus t
64	2026	60.1	3585	14	AEB96461	Aeb96461 Vesicular
65	2026	60.1	3921	14	AEB96460	Aeb96460 Heat shoc
66	2025.4	60.0	2109	6	ABL54023	Abl54023 Carcinoem
67	2025.4	60.0	2109	13	ADR89124	Adr89124 Human car
68	2015	59.7	2097	2	AAQ82807	Aaq82807 Carcinoem
69	2009.4	59.6	2106	4	AAH20121	Aah20121 Modified
70	2009.4	59.6	2106	5	AAD07347	Aad07347 Modified
71	2009.4	59.6	2106	10	ADE13860	Ade13860 CEA-CAP6D
72	2009.4	59.6	2106	14	ADZ58977	Adz58977 Novel CEA
73	2009.4	59.6	2106	14	AEB30767	Aeb30767 Multi-ant
c 74	2009.4	59.6	7958	6	AAI72490	Aai72490 H6-promot
75	2006.2	59.5	2106	6	AAI72489	Aai72489 CEA agoni
76	1977	58.6	2149	15	AEE91945	Aee91945 TatCEA fu
77	1975	58.6	2105	6	AAI72497	Aai72497 CEA agoni
78	1951.8	57.9	2907	10	ADD78270	Add78270 Human CGD
79	1945.4	57.7	2459	3	AAC77897	Aac77897 Human can
80	1932.8	57.3	2019	6	ABK86206	Abk86206 cDNA enco
81	1924.2	57.0	2059	2	AAT36495	Aat36495 Immunogen
82	1923.4	57.0	2349	13	ADT75840	Adt75840 Novel Fve
83	1889.4	56.0	2273	13	ADT50730	Adt50730 Cancer re
84	1843.6	54.7	1886	14	AEC79252	Aec79252 Human CEA
85	1843.6	54.7	1886	15	AEE80156	Aee80156 Human ova
86	1702.4	50.5	1943	4	AAH33528	Aah33528 Human col
87	1691.6	50.2	2364	11	ACN89142	Acn89142 Breast ca
88	1652.8	49.0	2118	13	ADR89123	Adr89123 Rhesus ca
89	1652.8	49.0	2118	13	ADR89119	Adr89119 Rhesus ca
90	1652.8	49.0	2118	14	AEB96450	Aeb96450 Rhesus mo
91	1652.8	49.0	2118	14	AEB96449	Aeb96449 Rhesus mo

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: August 9, 2006, 14:24:38 ; Search time 23345 Seconds
(without alignments)
8079.499 Million cell updates/sec

Title: US-10-553-436-36
Perfect score: 3373
Sequence: 1 ggaagagactcagggcagag.....tccagcctgggagacaaagt 3373

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1922.6	57.0	2588	6	CR749337	CR749337 Homo sapi
	2	1667	49.4	2109	14	DQ030270	DQ030270 Homo sapi
	3	1478	43.8	2109	14	DQ030271	DQ030271 Pan trogl
	4	883.6	26.2	3503	6	CR859350	CR859350 Pongo pyg
	5	872.8	25.9	1429	14	DQ046839	DQ046839 Homo sapi
	6	855.8	25.4	1429	14	DQ046840	DQ046840 Pan trogl
	7	841.2	24.9	904	3	BQ685640	BQ685640 AGENCOURT
	8	821.8	24.4	887	2	BI759915	BI759915 603044336
	9	803.8	23.8	841	5	CD618552	CD618552 56043850H
c	10	786.2	23.3	830	5	CD618551	CD618551 56043842J
c	11	771.4	22.9	792	5	CD618554	CD618554 56043858H
c	12	770.8	22.9	819	5	CD618548	CD618548 56043834H
	13	769.8	22.8	1015	2	BM471072	BM471072 AGENCOURT
	14	761	22.6	1386	6	CR608576	CR608576 full-leng
	15	758.2	22.5	958	14	DQ052381	DQ052381 Homo sapi
	16	755.6	22.4	823	5	CD618555	CD618555 56043858J
	17	743	22.0	904	9	DA760806	DA760806 DA760806
	18	738.8	21.9	1050	14	DQ046841	DQ046841 Homo sapi
	19	723	21.4	736	1	AL702861	AL702861 DKFZp686B
c	20	722.8	21.4	751	5	CD618553	CD618553 56043850J
c	21	716.4	21.2	727	5	CD618544	CD618544 56043734H
	22	711	21.1	969	8	CO579063	CO579063 ILLUMIGEN
	23	709.8	21.0	914	7	BE735665	BE735665 601304416
	24	704.2	20.9	803	5	CD618546	CD618546 56043758H
	25	702.8	20.8	726	5	CD618556	CD618556 56043910H
c	26	691.6	20.5	698	5	CD618547	CD618547 56043758J
	27	690.6	20.5	729	5	CD618558	CD618558 56044026H
	28	689.8	20.5	855	3	BP223131	BP223131 BP223131
c	29	669.6	19.9	712	5	CD618559	CD618559 56044026J
	30	668.6	19.8	876	3	BU195866	BU195866 AGENCOURT
	31	665	19.7	907	3	BQ689619	BQ689619 AGENCOURT
	32	662.2	19.6	716	5	CD618550	CD618550 56043842H
	33	657	19.5	700	3	BP223896	BP223896 BP223896
	34	645.6	19.1	823	5	CD618549	CD618549 56043834J
	35	645.4	19.1	767	3	BP223333	BP223333 BP223333
	36	645.2	19.1	940	3	BP223491	BP223491 BP223491
	37	641	19.0	853	3	BP223822	BP223822 BP223822
	38	638.4	18.9	651	1	AL602396	AL602396 DKFZp686F
	39	638	18.9	699	5	CD618508	CD618508 56019327H
	40	634.8	18.8	692	7	AW361899	AW361899 PM3-CT026
c	41	633.2	18.8	698	5	CD618509	CD618509 56019327J
	42	630.8	18.7	932	8	CO583711	CO583711 ILLUMIGEN
	43	629.8	18.7	691	2	BG986105	BG986105 PM2-DT004
	44	629.8	18.7	691	7	BF084846	BF084846 PM2-DT004
	45	629.4	18.7	958	14	DQ046842	DQ046842 Pan trogl
c	46	625.8	18.6	700	5	CD618517	CD618517 56019457J
c	47	622.8	18.5	661	5	CD618511	CD618511 56019433J
	48	622.2	18.4	790	9	DN998361	DN998361 TC118611
	49	622	18.4	630	4	BX480185	BX480185 DKFZp686F
	50	622	18.4	636	7	AW605345	AW605345 QV3-DT004
	51	617.8	18.3	677	5	CD618515	CD618515 56019449J
	52	616.2	18.3	794	8	CR629529	CR629529 DKFZp469A
	53	610.6	18.1	1026	3	BP223719	BP223719 BP223719
	54	610.4	18.1	796	2	BG768642	BG768642 602741968
	55	607.4	18.0	609	9	DB230447	DB230447 DB230447
	56	606	18.0	606	9	DA437137	DA437137 DA437137
	57	605.4	17.9	724	3	BM837491	BM837491 K-EST0113
	58	600	17.8	600	8	CV023132	CV023132 8539 Full
	59	600	17.8	616	5	CD618512	CD618512 56019441H
	60	599.4	17.8	601	3	BM786353	BM786353 K-EST0065
	61	597.4	17.7	600	9	DA440667	DA440667 DA440667
	62	597	17.7	597	9	DA441273	DA441273 DA441273
	63	596.8	17.7	600	9	DB201604	DB201604 DB201604
	64	595	17.6	595	1	AL602851	AL602851 DKFZp686P
	65	592.4	17.6	594	9	DB228961	DB228961 DB228961
	66	591.4	17.5	593	3	BM742895	BM742895 K-EST0015
	67	591	17.5	591	9	DB202268	DB202268 DB202268
	68	590.8	17.5	719	9	DR003971	DR003971 TC108044
	69	590.2	17.5	595	3	BP272385	BP272385 BP272385
	70	589.4	17.5	608	7	AW605337	AW605337 QV3-DT004
	71	589	17.5	589	7	AW936877	AW936877 RC1-DT002
	72	588	17.4	588	9	DB205882	DB205882 DB205882
	73	587.6	17.4	789	9	DN998502	DN998502 TC108168
	74	586.2	17.4	608	7	AW862419	AW862419 RC0-CT038
	75	586	17.4	611	7	AW860352	AW860352 RC0-CT038
	76	585	17.3	585	9	DB205913	DB205913 DB205913
	77	585	17.3	594	3	BP271979	BP271979 BP271979
	78	583.4	17.3	585	9	DA446657	DA446657 DA446657
	79	583	17.3	583	3	BP264343	BP264343 BP264343
	80	583	17.3	583	9	DB203715	DB203715 DB203715
	81	582.6	17.3	697	1	AL602318	AL602318 DKFZp686N
	82	582	17.3	582	3	BP293192	BP293192 BP293192
	83	582	17.3	582	9	DB202898	DB202898 DB202898
	84	582	17.3	583	9	DB203982	DB203982 DB203982
	85	581	17.2	581	9	DB206031	DB206031 DB206031
	86	581	17.2	582	3	BP329005	BP329005 BP329005
	87	580.6	17.2	587	3	BP293522	BP293522 BP293522
	88	580.4	17.2	582	9	DB010545	DB010545 DB010545
	89	580	17.2	580	9	DA766613	DA766613 DA766613
	90	579.2	17.2	597	3	BP272486	BP272486 BP272486
	91	578.6	17.2	586	3	BP220716	BP220716 BP220716
	92	578.4	17.1	580	3	BP261693	BP261693 BP261693

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: August 9, 2006, 14:14:45 ; Search time 18627 Seconds
(without alignments)
11579.677 Million cell updates/sec

Title: US-10-553-436-36
Perfect score: 3373
Sequence: 1 ggaagagactcagggcagag.....tccagcctgggagacaaagt 3373

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2780.8	82.4	3036	2	CQ800159	CQ800159 Sequence
2	2780.8	82.4	3036	5	HUMANTCE	M17303 Human carci
3	2681	79.5	2929	5	HUMCEA	M15042 Human carci
4	2680	79.5	2928	2	E01630	E01630 cDNA encodi
5	2680	79.5	2928	2	E13123	E13123 Human gene
6	2669.2	79.1	2974	2	CQ833969	CQ833969 Sequence
7	2669.2	79.1	2974	2	CQ981503	CQ981503 Sequence
8	2669.2	79.1	2974	2	CS017569	CS017569 Sequence
9	2669.2	79.1	2974	2	CS130722	CS130722 Sequence
10	2669.2	79.1	2974	2	DD161432	DD161432 EPITOPE S
11	2669.2	79.1	2974	2	AX332574	AX332574 Sequence
12	2669.2	79.1	2974	2	AX409670	AX409670 Sequence
13	2669.2	79.1	2974	2	AX658324	AX658324 Sequence
14	2669.2	79.1	2974	2	AX677147	AX677147 Sequence
15	2669.2	79.1	2974	2	AX805532	AX805532 Sequence
16	2669.2	79.1	2974	5	HUMCEAP	M29540 Human carci
17	2603.8	77.2	2888	5	BC034671	BC034671 Homo sapi
18	2552.6	75.7	2839	2	I08156	I08156 Sequence 2
19	2552.6	75.7	2839	2	I08166	I08166 Sequence 8
20	2261.8	67.1	2728	2	CQ413817	CQ413817 Sequence
21	2127.6	63.1	2359	5	AK223101	AK223101 Homo sapi
22	2115.8	62.7	2220	2	AR044683	AR044683 Sequence
23	2105.2	62.4	2350	7	BV177759	BV177759 sqnm96580
24	2027	60.1	2109	2	CQ947063	CQ947063 Sequence
25	2027	60.1	2109	2	AX133977	AX133977 Sequence
26	2027	60.1	2109	2	AX468838	AX468838 Sequence
27	2027	60.1	2167	2	CS148786	CS148786 Sequence
28	2027	60.1	2349	2	AR052808	AR052808 Sequence
29	2027	60.1	2349	2	AR288121	AR288121 Sequence
30	2027	60.1	2349	2	AR567108	AR567108 Sequence
31	2027	60.1	2434	2	AR052807	AR052807 Sequence
32	2027	60.1	2434	2	AR288120	AR288120 Sequence
33	2027	60.1	2434	2	AR567107	AR567107 Sequence
34	2026	60.1	2031	2	A39900	A39900 Sequence 2
35	2026	60.1	2031	2	I67748	I67748 Sequence 2
36	2026	60.1	2037	2	CS148782	CS148782 Sequence
37	2026	60.1	2355	2	CS148769	CS148769 Sequence
38	2026	60.1	2766	2	CS148767	CS148767 Sequence
39	2026	60.1	2857	2	CS148809	CS148809 Sequence
40	2026	60.1	3426	2	CS148784	CS148784 Sequence
41	2026	60.1	3585	2	CS148788	CS148788 Sequence
42	2026	60.1	3921	2	CS148787	CS148787 Sequence
43	2025.4	60.0	2109	2	CQ859390	CQ859390 Sequence
44	2015	59.7	2097	2	A43169	A43169 Sequence 35
45	2015	59.7	2097	2	AR079553	AR079553 Sequence
46	2009.4	59.6	2106	2	CS141685	CS141685 Sequence
47	2009.4	59.6	2106	2	AX133657	AX133657 Sequence
48	2009.4	59.6	2106	2	AX192349	AX192349 Sequence
49	2000	59.3	2092	5	HSCEAASP	X16455 Human mRNA
50	1987	58.9	2106	2	AX393888	AX393888 Sequence
51	1932.8	57.3	2019	2	AX505112	AX505112 Sequence
52	1923.4	57.0	2349	2	CQ898819	CQ898819 Sequence
53	1652.8	49.0	2118	2	CQ859385	CQ859385 Sequence
54	1652.8	49.0	2118	2	CQ859389	CQ859389 Sequence
55	1652.8	49.0	2118	2	CS148776	CS148776 Sequence
56	1652.8	49.0	2118	2	CS148777	CS148777 Sequence
57	1618.2	48.0	2547	2	CQ413250	CQ413250 Sequence
58	1292.4	38.3	2034	2	CQ947075	CQ947075 Sequence
59	1292.4	38.3	2109	2	CQ947061	CQ947061 Sequence
60	1292.4	38.3	2355	2	CS148771	CS148771 Sequence
61	1292.4	38.3	2358	2	CS148772	CS148772 Sequence
62	1292.4	38.3	2859	2	CS148781	CS148781 Sequence
63	1231.4	36.5	2059	2	AX805534	AX805534 Sequence
64	1230.6	36.5	2167	2	AX805536	AX805536 Sequence
65	1229.2	36.4	39707	5	AC008999	AC008999 Homo sapi
66	1191.2	35.3	2664	2	CS148785	CS148785 Sequence
67	1174	34.8	1422	5	HUMCEAX	M16234 Human carci
68	1106.8	32.8	2140	2	AX805538	AX805538 Sequence
69	1103	32.7	2155	2	AX805540	AX805540 Sequence
70	1073.8	31.8	2118	2	CS047791	CS047791 Sequence
71	1073.8	31.8	2358	2	CS148774	CS148774 Sequence
72	1073.8	31.8	2359	2	CS148812	CS148812 Sequence
73	1073.8	31.8	2859	2	CS148810	CS148810 Sequence
74	1065	31.6	1623	2	AX497809	AX497809 Sequence
75	959.8	28.5	1054	5	HUMCEA09	M59709 Human carci
76	912.4	27.1	1630	2	I08160	I08160 Sequence 10
77	912.4	27.1	1630	2	I08163	I08163 Sequence 3
78	912.4	27.1	1636	5	BC014473	BC014473 Homo sapi
79	912.4	27.1	2197	5	HUMBGPI	J03858 Human bilia
80	912.4	27.1	3461	2	I08157	I08157 Sequence 4
81	912.4	27.1	3461	2	I08167	I08167 Sequence 10
82	912.4	27.1	3464	2	CQ834029	CQ834029 Sequence
83	912.4	27.1	3464	2	CQ875303	CQ875303 Sequence
84	912.4	27.1	3464	2	AX330303	AX330303 Sequence
85	912.4	27.1	3464	2	AX818143	AX818143 Sequence
86	912.4	27.1	3464	5	HSTM1CEA	X16354 Human mRNA
87	910.8	27.0	1742	5	HUMBGP1	D90311 Homo sapien
88	910.8	27.0	1760	2	E03350	E03350 cDNA sequen
89	910.8	27.0	1773	5	HUMBGPAB	M72238 Human bilia
90	909.2	27.0	3446	5	HSM804897	AL833584 Homo sapi
91	902	26.7	1653	5	BC024164	BC024164 Homo sapi

Sequence Alignment between SEQ ID NO:36 and SEQ ID NO:52

```
Db       3301 GGCATGAACCCGGGAGGCAGGGCTTGCAGTGAGCCAAGATCATGCCGCTGCACTCCAGCC 3360

Qy       3361 TGGGAGACAAAGT 3373
              |||||||||||||
Db       3361 TGGGAGACAAAGT 3373
```

RESULT 4
US-10-558-861-52
; Sequence 52, Application US/10558861
; GENERAL INFORMATION:
; APPLICANT: diaDexus, inc.
; APPLICANT: Macina, Roberto
; APPLICANT: Turner, Leah
; APPLICANT: Sun, Yongming
; TITLE OF INVENTION: Compositions, Splice Variants and Methods Relating to Ovarian Spe
; TITLE OF INVENTION: Nucleic Acids and Proteins
; FILE REFERENCE: DEX-0487
; CURRENT APPLICATION NUMBER: US/10/558,861
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: US 60/474,856
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 3373
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-558-861-52

Query Match 100.0%; Score 3373; DB 51; Length 3373;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGAAGAGACTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGAAGAGACTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGA 60

Qy         61 CAAAACGTTCCTGGAACTCAAGCTCTTCTCCACAGAGGAGGACAGAGCAGACAGCAGAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAAAACGTTCCTGGAACTCAAGCTCTTCTCCACAGAGGAGGACAGAGCAGACAGCAGAGA 120

Qy        121 CCATGGAGTCTCCCTCGGCCCCTCCCCACAGATGGTGCATCCCCTGGCAGAGGCTCCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCATGGAGTCTCCCTCGGCCCCTCCCCACAGATGGTGCATCCCCTGGCAGAGGCTCCTGC 180

Qy        181 TCACAGCCTCACTTCTAACCTTCTGGAACCCGCCCACCACTGCCAAGCTCACTATTGAAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACAGCCTCACTTCTAACCTTCTGGAACCCGCCCACCACTGCCAAGCTCACTATTGAAT 240

Qy        241 CCACGCCGTTCAATGTCGCAGAGGGGAAGGAGGTGCTTCTACTTGTCCACAATCTGCCCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCACGCCGTTCAATGTCGCAGAGGGGAAGGAGGTGCTTCTACTTGTCCACAATCTGCCCC 300

Qy        301 AGCATCTTTTTGGCTACAGCTGGTACAAAGGTGAAAGAGTGGATGGCAACCGTCAAATTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGCATCTTTTTGGCTACAGCTGGTACAAAGGTGAAAGAGTGGATGGCAACCGTCAAATTA 360

Qy        361 TAGGATATGTAATAGGAACTCAACAAGCTACCCCAGGGCCCGCATACAGTGGTCGAGAGA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TAGGATATGTAATAGGAACTCAACAAGCTACCCCAGGGCCCGCATACAGTGGTCGAGAGA 420

Qy        421 TAATATACCCCAATGCATCCCTGCTGATCCAGAACATCATCCAGAATGACACAGGATTCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATATACCCCAATGCATCCCTGCTGATCCAGAACATCATCCAGAATGACACAGGATTCT 480

Qy        481 ACACCCTACACGTCATAAAGTCAGATCTTGTGAATGAAGAAGCAACTGGCCAGTTCCGGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACACCCTACACGTCATAAAGTCAGATCTTGTGAATGAAGAAGCAACTGGCCAGTTCCGGG 540

Qy        541 TATACCCGGAGCTGCCCAAGCCCTCCATCTCCAGCAACAACTCCAAACCCGTGGAGGACA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TATACCCGGAGCTGCCCAAGCCCTCCATCTCCAGCAACAACTCCAAACCCGTGGAGGACA 600

Qy        601 AGGATGCTGTGGCCTTCACCTGTGAACCTGAGACTCAGGACGCAACCTACCTGTGGTGGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGGATGCTGTGGCCTTCACCTGTGAACCTGAGACTCAGGACGCAACCTACCTGTGGTGGG 660

Qy        661 TAAACAATCAGAGCCTCCCGGTCAGTCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TAAACAATCAGAGCCTCCCGGTCAGTCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCC 720

Qy        721 TCACTCTATTCAATGTCACAAGAAATGACACAGCAAGCTACAAATGTGAAACCCAGAACC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCACTCTATTCAATGTCACAAGAAATGACACAGCAAGCTACAAATGTGAAACCCAGAACC 780

Qy        781 CAGTGAGTGCCAGGCGCAGTGATTCAGTCATCCTGAATGTCCTCTATGGCCCGGATGCCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGTGAGTGCCAGGCGCAGTGATTCAGTCATCCTGAATGTCCTCTATGGCCCGGATGCCC 840

Qy        841 CCACCATTTCCCCTCTAAACACATCTTACAGATCAGGGGAAAATCTGAACCTCTCCTGCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCACCATTTCCCCTCTAAACACATCTTACAGATCAGGGGAAAATCTGAACCTCTCCTGCC 900

Qy        901 ACGCAGCCTCTAACCCACCTGCACAGTACTCTTGGTTTGTCAATGGGACTTTCCAGCAAT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ACGCAGCCTCTAACCCACCTGCACAGTACTCTTGGTTTGTCAATGGGACTTTCCAGCAAT 960

Qy        961 CCACCCAAGAGCTCTTTATCCCCAACATCACTGTGAATAATAGTGGATCCTATACGTGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCACCCAAGAGCTCTTTATCCCCAACATCACTGTGAATAATAGTGGATCCTATACGTGCC 1020

Qy       1021 AAGCCCATAACTCAGACACTGGCCTCAATAGGACCACAGTCACGACGATCACAGTCTATG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAGCCCATAACTCAGACACTGGCCTCAATAGGACCACAGTCACGACGATCACAGTCTATG 1080

Qy       1081 CAGAGCCACCCAAACCCTTCATCACCAGCAACAACTCCAACCCCGTGGAGGATGAGGATG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAGAGCCACCCAAACCCTTCATCACCAGCAACAACTCCAACCCCGTGGAGGATGAGGATG 1140

Qy       1141 CTGTAGCCTTAACCTGTGAACCTGAGATTCAGAACACAACCTACCTGTGGTGGGTAAATA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTGTAGCCTTAACCTGTGAACCTGAGATTCAGAACACAACCTACCTGTGGTGGGTAAATA 1200

Qy       1201 ATCAGAGCCTCCCGGTCAGTCCCAGGCTGCAGCTGTCCAATGACAACAGGACCCTCACTC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ATCAGAGCCTCCCGGTCAGTCCCAGGCTGCAGCTGTCCAATGACAACAGGACCCTCACTC 1260

Qy       1261 TACTCAGTGTCACAAGGAATGATGTAGGACCCTATGAGTGTGGAATCCAGAACGAATTAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACTCAGTGTCACAAGGAATGATGTAGGACCCTATGAGTGTGGAATCCAGAACGAATTAA 1320

Qy       1321 GTGTTGACCACAGCGACCCAGTCATCCTGAATGTCCTCTATGGCCCAGACGACCCCACCA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GTGTTGACCACAGCGACCCAGTCATCCTGAATGTCCTCTATGGCCCAGACGACCCCACCA 1380

Qy       1381 TTTCCCCCTCATACACCTATTACCGTCCAGGGGTGAACCTCAGCCTCTCCTGCCATGCAG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTCCCCCTCATACACCTATTACCGTCCAGGGGTGAACCTCAGCCTCTCCTGCCATGCAG 1440

Qy       1441 CCTCTAACCCACCTGCACAGTATTCTTGGCTGATTGATGGGAACATCCAGCAACACACAC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCTCTAACCCACCTGCACAGTATTCTTGGCTGATTGATGGGAACATCCAGCAACACACAC 1500

Qy       1501 AAGAGCTCTTTATCTCCAACATCACTGAGAAGAACAGCGGACTCTATACCTGCCAGGCCA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AAGAGCTCTTTATCTCCAACATCACTGAGAAGAACAGCGGACTCTATACCTGCCAGGCCA 1560

Qy       1561 ATAACTCAGCCAGTGGCCACAGCAGGACTACAGTCAAGACAATCACAGTCTCTGCGGAGC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATAACTCAGCCAGTGGCCACAGCAGGACTACAGTCAAGACAATCACAGTCTCTGCGGAGC 1620

Qy       1621 TGCCCAAGCCCTCCATCTCCAGCAACAACTCCAAACCCGTGGAGGACAAGGATGCTGTGG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TGCCCAAGCCCTCCATCTCCAGCAACAACTCCAAACCCGTGGAGGACAAGGATGCTGTGG 1680
```

```
Qy       1681 CCTTCACCTGTGAACCTGAGGCTCAGAACACAACCTACCTGTGGTGGGTAAATGGTCAGA 1740
Db       1681 CCTTCACCTGTGAACCTGAGGCTCAGAACACAACCTACCTGTGGTGGGTAAATGGTCAGA 1740

Qy       1741 GCCTCCCAGTCAGTCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTATTCA 1800
Db       1741 GCCTCCCAGTCAGTCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTATTCA 1800

Qy       1801 ATGTCACAAGAAATGACGCAAGAGCCTATGTATGTGGAATCCAGAACTCAGTGAGTGCAA 1860
Db       1801 ATGTCACAAGAAATGACGCAAGAGCCTATGTATGTGGAATCCAGAACTCAGTGAGTGCAA 1860

Qy       1861 ACCGCAGTGACCCAGTCACCCTGGATGTCCTCTATGGGCCGGACACCCCCATCATTTCCC 1920
Db       1861 ACCGCAGTGACCCAGTCACCCTGGATGTCCTCTATGGGCCGGACACCCCCATCATTTCCC 1920

Qy       1921 CCCCAGACTCGTCTTACCTTTCGGGAGCGAACCTCAACCTCTCCTGCCACTCGGCCTCTA 1980
Db       1921 CCCCAGACTCGTCTTACCTTTCGGGAGCGAACCTCAACCTCTCCTGCCACTCGGCCTCTA 1980

Qy       1981 ACCCATCCCCCGCAGTATTCTTGGCGTATCAATGGGATACCGCAGCAACACACACAAGTTC 2040
Db       1981 ACCCATCCCCCGCAGTATTCTTGGCGTATCAATGGGATACCGCAGCAACACACACAAGTTC 2040

Qy       2041 TCTTTATCGCCAAAATCACGCCAAATAATAACGGGACCTATGCCTGTTTTGTCTCTAACT 2100
Db       2041 TCTTTATCGCCAAAATCACGCCAAATAATAACGGGACCTATGCCTGTTTTGTCTCTAACT 2100

Qy       2101 TGGCTACTGGCCGCAATAATTCCATAGTCAAGAGCATCACAGTCTCTGACAGTTGTTTTG 2160
Db       2101 TGGCTACTGGCCGCAATAATTCCATAGTCAAGAGCATCACAGTCTCTGACAGTTGTTTTG 2160

Qy       2161 CTTCTTCCTTAAAGCATTTGCAACAGCTACAGTCTAAAATTGCTTCTTTACCAAGGATAT 2220
Db       2161 CTTCTTCCTTAAAGCATTTGCAACAGCTACAGTCTAAAATTGCTTCTTTACCAAGGATAT 2220

Qy       2221 TTACAGAAAAGACTCTGACCAGAGATCGAGACCATCCTAGCCAACATCGTGAAACCCCAT 2280
Db       2221 TTACAGAAAAGACTCTGACCAGAGATCGAGACCATCCTAGCCAACATCGTGAAACCCCAT 2280

Qy       2281 CTCTACTAAAAATACAAAAATGAGCTGGGCTTGGTGGCGCGCACCTGTAGTCCCAGTTAC 2340
Db       2281 CTCTACTAAAAATACAAAAATGAGCTGGGCTTGGTGGCGCGCACCTGTAGTCCCAGTTAC 2340

Qy       2341 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGAGATTGCAGTGAGCCCA 2400
Db       2341 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGAGATTGCAGTGAGCCCA 2400

Qy       2401 GATCGCACCACTGCACTCCAGTCTGGCAACAGAGCAAGACTCCATCTCAAAAAGAAAAGA 2460
Db       2401 GATCGCACCACTGCACTCCAGTCTGGCAACAGAGCAAGACTCCATCTCAAAAAGAAAAGA 2460

Qy       2461 AAAGAAGACTCTGACCTGTACTCTTGAATACAAGTTTCTGATACCACTGCACTGTCTGAG 2520
Db       2461 AAAGAAGACTCTGACCTGTACTCTTGAATACAAGTTTCTGATACCACTGCACTGTCTGAG 2520

Qy       2521 AATTTCCAAAACTTTAATGAACTAACTGACAGCTTCATGAAACTGTCCACCAAGATCAAG 2580
Db       2521 AATTTCCAAAACTTTAATGAACTAACTGACAGCTTCATGAAACTGTCCACCAAGATCAAG 2580

Qy       2581 CAGAGAAAATAATTAATTTCATGGGACTAAATGAACTAATGAGGATAATATTTTCATAAT 2640
Db       2581 CAGAGAAAATAATTAATTTCATGGGACTAAATGAACTAATGAGGATAATATTTTCATAAT 2640

Qy       2641 TTTTTATTTGAAATTTTGCTGATTCTTTAAATGTCTTGTTTCCCAGATTTCAGGAAACTT 2700
Db       2641 TTTTTATTTGAAATTTTGCTGATTCTTTAAATGTCTTGTTTCCCAGATTTCAGGAAACTT 2700

Qy       2701 TTTTTCTTTTAAGCTATCCACAGCTTACAGCAATTTGATAAAATATACTTTTGTGAACAA 2760
Db       2701 TTTTTCTTTTAAGCTATCCACAGCTTACAGCAATTTGATAAAATATACTTTTGTGAACAA 2760

Qy       2761 AAATTGAGACATTTACATTTTCTCCCTATGTGGTCGCTCCAGACTTGGGAAACTATTCAT 2820
Db       2761 AAATTGAGACATTTACATTTTCTCCCTATGTGGTCGCTCCAGACTTGGGAAACTATTCAT 2820

Qy       2821 GAATATTTATATTGTATGGTAATATAGTTATTGCACAAGTTCAATAAAAATCTGCTCTTT 2880
Db       2821 GAATATTTATATTGTATGGTAATATAGTTATTGCACAAGTTCAATAAAAATCTGCTCTTT 2880

Qy       2881 GTATGACAGAATACATTTGAAAACATTGGTTATATTACCAAGACTTTGACTAGAATGTCG 2940
Db       2881 GTATGACAGAATACATTTGAAAACATTGGTTATATTACCAAGACTTTGACTAGAATGTCG 2940

Qy       2941 TATTTGAGGATATAAACCCATAGGTAATAAACCCACAGGTACTACAAACAAAGTCTGAAG 3000
Db       2941 TATTTGAGGATATAAACCCATAGGTAATAAACCCACAGGTACTACAAACAAAGTCTGAAG 3000

Qy       3001 TCAGCCTTGGTTTGGCTTCCTAGTGTCAATTAAACTTCTAAAAGTTTAATCTGAGATTCC 3060
Db       3001 TCAGCCTTGGTTTGGCTTCCTAGTGTCAATTAAACTTCTAAAAGTTTAATCTGAGATTCC 3060

Qy       3061 TTATAAAAACTTCCAGCAAAGCAACTTTAAAAAAGTCTGTGTGGGCCGGGCGCGGTGGCT 3120
Db       3061 TTATAAAAACTTCCAGCAAAGCAACTTTAAAAAAGTCTGTGTGGGCCGGGCGCGGTGGCT 3120

Qy       3121 CACGCCTGTAATCCCAGCACTTTGATCCGCCGAGGCGGGCGGATCACGAGGTCAGGAGAT 3180
Db       3121 CACGCCTGTAATCCCAGCACTTTGATCCGCCGAGGCGGGCGGATCACGAGGTCAGGAGAT 3180

Qy       3181 CCAGACCATCCTGGCTAACACAGTGAAACCCCGTCTCTACTAAAAATACAAAAAAAGTTA 3240
Db       3181 CCAGACCATCCTGGCTAACACAGTGAAACCCCGTCTCTACTAAAAATACAAAAAAAGTTA 3240

Qy       3241 GCCGGGCGTGGTGGTGGGGGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAC 3300
Db       3241 GCCGGGCGTGGTGGTGGGGGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAC 3300

Qy       3301 GGCATGAACCCGGGAGGCAGGGCTTGCAGTGAGCCAAGATCATGCCGCTGCACTCCAGCC 3360
Db       3301 GGCATGAACCCGGGAGGCAGGGCTTGCAGTGAGCCAAGATCATGCCGCTGCACTCCAGCC 3360

Qy       3361 TGGGAGACAAAGT 3373
Db       3361 TGGGAGACAAAGT 3373
```

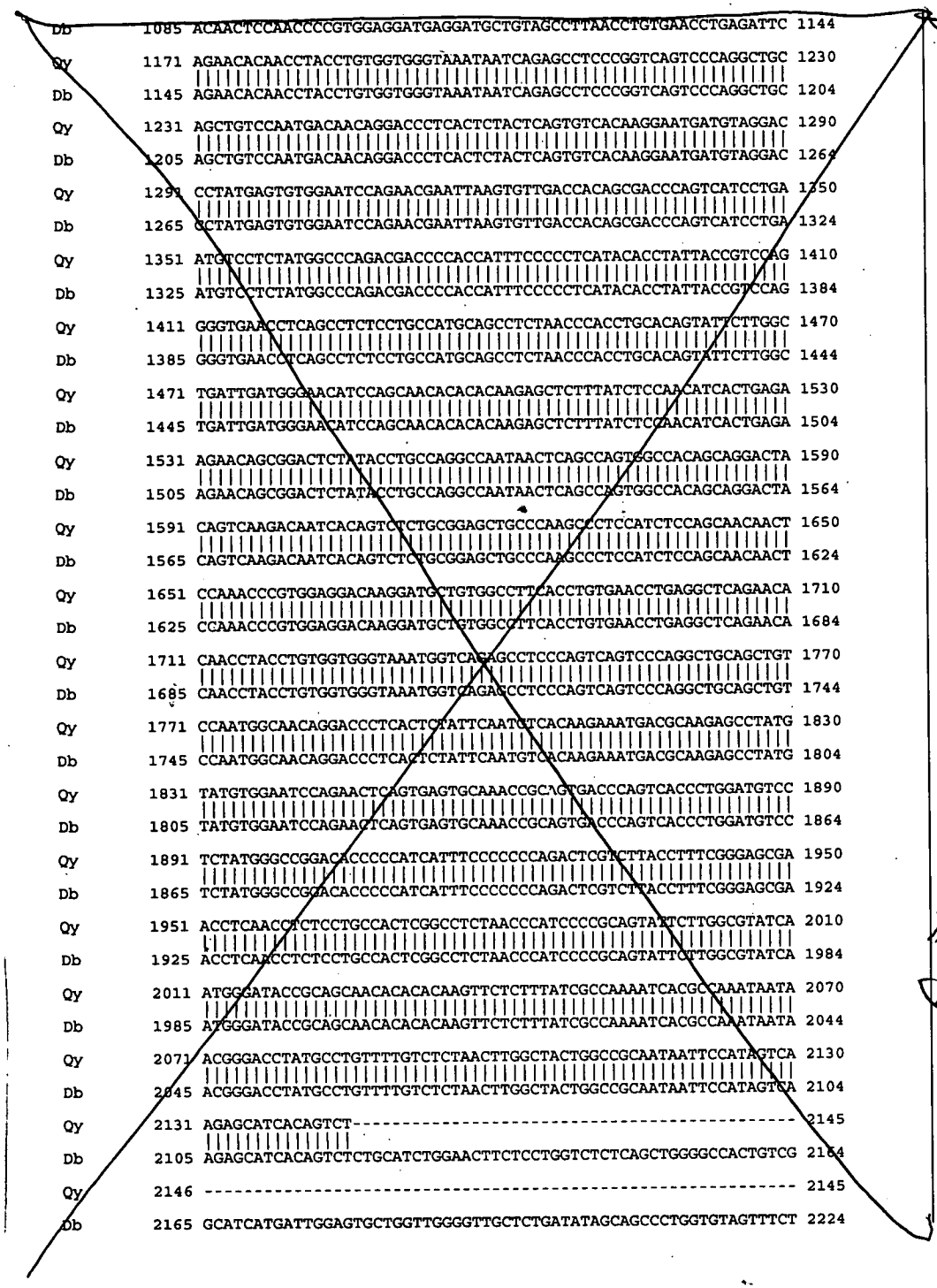
```
RESULT 5
US-11-050-875-808
; Sequence 808, Application US/11050875
; GENERAL INFORMATION:
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHOD
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 1847.1001
;  CURRENT APPLICATION NUMBER: US/11/050,875
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1583
; SEQ ID NO 808
;   LENGTH: 3470
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-050-875-808

  Query Match           96.7%;  Score 3261.4;  DB 65;  Length 3470;
  Best Local Similarity  97.3%;  Pred. No. 0;
  Matches 3364;  Conservative    0;  Mismatches    1;  Indels   92;  Gaps    1;

Qy          9 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 68
Db          1 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 60

Qy         69 TCCTGGAACTCAAGCTCTTCTCCACAGAGGAGGACAGAGCAGACAGCAGAGACCATGGAG 128
Db         61 TCCTGGAACTCAAGCTCTTCTCCACAGAGGAGGACAGAGCAGACAGCAGAGACCATGGAG 120
```

Sequence Alignment between SEQ ID NO:36 and M15047



RESULT 3
HUMCEA
LOCUS HUMCEA 2929 bp mRNA linear PRI 01-NOV-1994
DEFINITION Human carcinoembryonic antigen mRNA.
ACCESSION M15042
VERSION M15042.1 GI:180198
KEYWORDS Alu repeat; antigen; carcinoembryonic antigen; repeat region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2929)
AUTHORS Oikawa,S., Nakazato,H. and Kosaki,G.
TITLE Primary structure of human carcinoembryonic antigen (CEA) deduced

```
            from cDNA sequence
  JOURNAL   Biochem. Biophys. Res. Commun. 142 (2), 511-518 (1987)
    PUBMED  3814146
  COMMENT   Original source text: Human malignant colon tissue, cDNA to mRNA,
            clones pCEA[55-2,80-11].
            Clean copy of sequence [1] kindly provided by S.Oikawa
            (25-MAR-1987).
  FEATURES             Location/Qualifiers
       source          1. .2929
                       /organism="Homo sapiens"
                       /mol_type="mRNA"
                       /db_xref="taxon:9606"
                       /map="19q13.2"
       gene            1. .2929
                       /gene="CEA"
       mRNA            <1. .2876
                       /gene="CEA"
                       /product="CEA mRNA"
       CDS             <1. .2099
                       /gene="CEA"
                       /note="carcinoembryonic antigen precursor"
                       /codon_start=2
                       /protein_id="AAA51963.1"
                       /db_xref="GI:180199"
                       /db_xref="GDB:G00-119-054"
                       /translation="SAPPHRWCIPWQRLLLTASLLTFWNPPTTAKLTIESTPFNVAEG
                       KEVLLLVHNLPQHLFGYSWYKGERVDGNRQIIGYVIGTQQATPGPAYSGREIIYPNAS
                       LLIQNIIQNDTGFYTLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKPVEDKDAVA
                       FTCEPETQDATYLWWVNNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASYKCETQNPVS
                       ARRSDSVILNVLYGPDAPTISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQQS
                       TQELFIPNITVNNSGSYTCQAHNSDTGLNRTTVTTITVYAEPPKPFITSNNSNPVEDE
                       DAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLLSVTRNDVGPYECGIQ
                       NELSVDHSDPVILNVLYGPDDPTISPSYTYYRPGVNLSLSCHAASNPPAQYSWLIDGN
                       IQQHTQELFISNITEKNSGLYTCQANNSASGHSRTTVKTITVSAELPKPSISSNNSKP
                       VEDKDAVAFTCEPEAQNTTYLWWVNGQSLPVSPRLQLSNGNRTLTLFNVTRNDARAYV
                       CGIQNSVSANRSDPVTLDVLYGPDTPIISPPDSSYLSGANLNLSCHSASNPSPQYSWR
                       INGIPQQHTQVLFIAKITPNNNGTYACFVSNLATGRNNSIVKSITVSASGTSPGLSAG
                       ATVGIMIGVLVGVALI"
       sig_peptide     <1. .91
                       /gene="CEA"
                       /note="carcinoembryonic antigen signal peptide"
       mat_peptide     92. .2095
                       /gene="CEA"
                       /product="carcinoembryonic antigen"
       repeat_region   2215. .2462
                       /note="truncated Alu repeat"
  ORIGIN      185 bp upstream of PvuII site.

    Query Match             79.5%;  Score 2681;  DB 5;  Length 2929;
    Best Local Similarity   95.9%;  Pred. No. 0;
    Matches 2810;  Conservative    0;  Mismatches    0;  Indels  119;  Gaps    1;

Qy      134 CTCGGCCCCTCCCCACAGATGGTGCATCCCCTGGCAGAGGCTCCTGCTCACAGCCTCACT 193
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 CTCGGCCCCTCCCCACAGATGGTGCATCCCCTGGCAGAGGCTCCTGCTCACAGCCTCACT  60

Qy      194 TCTAACCTTCTGGAACCCGCCCACCACTGCCAAGCTCACTATTGAATCCACGCCGTTCAA 253
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCTAACCTTCTGGAACCCGCCCACCACTGCCAAGCTCACTATTGAATCCACGCCGTTCAA 120

Qy      254 TGTCGCAGAGGGGAAGGAGGTGCTTCTACTTGTCCACAATCTGCCCCAGCATCTTTTTGG 313
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TGTCGCAGAGGGGAAGGAGGTGCTTCTACTTGTCCACAATCTGCCCCAGCATCTTTTTGG 180

Qy      314 CTACAGCTGGTACAAAGGTGAAAGAGTGGATGGCAACCGTCAAATTATAGGATATGTAAT 373
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTACAGCTGGTACAAAGGTGAAAGAGTGGATGGCAACCGTCAAATTATAGGATATGTAAT 240

Qy      374 AGGAACTCAACAAGCTACCCCAGGGCCCGCATACAGTGGTCGAGAGATAATATACCCCAA 433
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 AGGAACTCAACAAGCTACCCCAGGGCCCGCATACAGTGGTCGAGAGATAATATACCCCAA 300

Qy      434 TGCATCCCTGCTGATCCAGAACATCATCCAGAATGACACAGGATTCTACACCCTACACGT 493
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 TGCATCCCTGCTGATCCAGAACATCATCCAGAATGACACAGGATTCTACACCCTACACGT 360

Qy      494 CATAAAGTCAGATCTTGTGAATGAAGAAGCAACTGGCCAGTTCCGGGTATACCCGGAGCT 553
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CATAAAGTCAGATCTTGTGAATGAAGAAGCAACTGGCCAGTTCCGGGTATACCCGGAGCT 420

Qy      554 GCCCAAGCCCTCCATCTCCAGCAACAACTCCAAACCCGTGGAGGACAAGGATGCTGTGGC 613
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GCCCAAGCCCTCCATCTCCAGCAACAACTCCAAACCCGTGGAGGACAAGGATGCTGTGGC 480

Qy      614 CTTCACCTGTGAACCTGAGACTCAGGACGCAACCTACCTGTGGTGGGTAAACAATCAGAG 673
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CTTCACCTGTGAACCTGAGACTCAGGACGCAACCTACCTGTGGTGGGTAAACAATCAGAG 540

Qy      674 CCTCCCGGTCAGTCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTATTCAA 733
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CCTCCCGGTCAGTCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTATTCAA 600

Qy      734 TGTCACAAGAAATGACACAGCAAGCTACAAATGTGAAACCCAGAACCCAGTGAGTGCCAG 793
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TGTCACAAGAAATGACACAGCAAGCTACAAATGTGAAACCCAGAACCCAGTGAGTGCCAG 660

Qy      794 GCGCAGTGATTCAGTCATCCTGAATGTCCTCTATGGCCCGGATGCCCCCACCATTTCCCC 853
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 GCGCAGTGATTCAGTCATCCTGAATGTCCTCTATGGCCCGGATGCCCCCACCATTTCCCC 720

Qy      854 TCTAAACACATCTTACAGATCAGGGGAAAATCTGAACCTCTCCTGCCACGCAGCCTCTAA 913
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TCTAAACACATCTTACAGATCAGGGGAAAATCTGAACCTCTCCTGCCACGCAGCCTCTAA 780

Qy      914 CCCACCTGCACAGTACTCTTGGTTTGTCAATGGGACTTTCCAGCAATCCACCCAAGAGCT 973
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 CCCACCTGCACAGTACTCTTGGTTTGTCAATGGGACTTTCCAGCAATCCACCCAAGAGCT 840

Qy      974 CTTTATCCCCAACATCACTGTGAATAATAGTGGATCCTATACGTGCCAAGCCCATAACTC 1033
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 CTTTATCCCCAACATCACTGTGAATAATAGTGGATCCTATACGTGCCAAGCCCATAACTC 900

Qy     1034 AGACACTGGCCTCAATAGGACCACAGTCACGACGATCACAGTCTATGCAGAGCCACCCAA 1093
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 AGACACTGGCCTCAATAGGACCACAGTCACGACGATCACAGTCTATGCAGAGCCACCCAA 960

Qy     1094 ACCCTTCATCACCAGCAACAACTCCAACCCCGTGGAGGATGAGGATGCTGTAGCCTTAAC 1153
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 ACCCTTCATCACCAGCAACAACTCCAACCCCGTGGAGGATGAGGATGCTGTAGCCTTAAC 1020

Qy     1154 CTGTGAACCTGAGATTCAGAACACAACCTACCTGTGGTGGGTAAATAATCAGAGCCTCCC 1213
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 CTGTGAACCTGAGATTCAGAACACAACCTACCTGTGGTGGGTAAATAATCAGAGCCTCCC 1080

Qy     1214 GGTCAGTCCCAGGCTGCAGCTGTCCAATGACAACAGGACCCTCACTCTACTCAGTGTCAC 1273
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 GGTCAGTCCCAGGCTGCAGCTGTCCAATGACAACAGGACCCTCACTCTACTCAGTGTCAC 1140

Qy     1274 AAGGAATGATGTAGGACCCTATGAGTGTGGAATCCAGAACGAATTAAGTGTTGACCACAG 1333
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 AAGGAATGATGTAGGACCCTATGAGTGTGGAATCCAGAACGAATTAAGTGTTGACCACAG 1200

Qy     1334 CGACCCAGTCATCCTGAATGTCCTCTATGGCCCAGACGACCCCACCATTTCCCCCTCATA 1393
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 CGACCCAGTCATCCTGAATGTCCTCTATGGCCCAGACGACCCCACCATTTCCCCCTCATA 1260

Qy     1394 CACCTATTACCGTCCAGGGGTGAACCTCAGCCTCTCCTGCCATGCAGCCTCTAACCCACC 1453
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 CACCTATTACCGTCCAGGGGTGAACCTCAGCCTCTCCTGCCATGCAGCCTCTAACCCACC 1320

Qy     1454 TGCACAGTATTCTTGGCTGATTGATGGGAACATCCAGCAACACACACAAGAGCTCTTTAT 1513
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 TGCACAGTATTCTTGGCTGATTGATGGGAACATCCAGCAACACACACAAGAGCTCTTTAT 1380

Qy     1514 CTCCAACATCACTGAGAAGAACAGCGGACTCTATACCTGCCAGGCCAATAACTCAGCCAG 1573
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      1381 CTCCAACATCACTGAGAAGAACAGCGGACTCTATACCTGCCAGGCCAATAACTCAGCCAG 1440
Qy      1574 TGGCCACAGCAGGACTACAGTCAAGACAATCACAGTCTCTGCGGAGCTGCCCAAGCCCTC 1633
Db      1441 TGGCCACAGCAGGACTACAGTCAAGACAATCACAGTCTCTGCGGAGCTGCCCAAGCCCTC 1500
Qy      1634 CATCTCCAGCAACAACTCCAAACCCGTGGAGGACAAGGATGCTGTGGCCTTCACCTGTGA 1693
Db      1501 CATCTCCAGCAACAACTCCAAACCCGTGGAGGACAAGGATGCTGTGGCCTTCACCTGTGA 1560
Qy      1694 ACCTGAGGCTCAGAACACAACCTACCTGTGGTGGGTAAATGGTCAGAGCCTCCCAGTCAG 1753
Db      1561 ACCTGAGGCTCAGAACACAACCTACCTGTGGTGGGTAAATGGTCAGAGCCTCCCAGTCAG 1620
Qy      1754 TCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTATTCAATGTCACAAGAAA 1813
Db      1621 TCCCAGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTATTCAATGTCACAAGAAA 1680
Qy      1814 TGACGCAAGAGCCTATGTATGTGGAATCCAGAACTCAGTGAGTGCAAACCGCAGTGACCC 1873
Db      1681 TGACGCAAGAGCCTATGTATGTGGAATCCAGAACTCAGTGAGTGCAAACCGCAGTGACCC 1740
Qy      1874 AGTCACCCTGGATGTCCTCTATGGGCCGGACACCCCCATCATTTCCCCCCCAGACTCGTC 1933
Db      1741 AGTCACCCTGGATGTCCTCTATGGGCCGGACACCCCCATCATTTCCCCCCCAGACTCGTC 1800
Qy      1934 TTACCTTTCGGGAGCGAACCTCAACCTCTCCTGCCACTCGGCCTCTAACCCATCCCCGCA 1993
Db      1801 TTACCTTTCGGGAGCGAACCTCAACCTCTCCTGCCACTCGGCCTCTAACCCATCCCCGCA 1860
Qy      1994 GTATTCTTGGCGTATCAATGGGATACCGCAGCAACACACACAAGTTCTCTTTATCGCCAA 2053
Db      1861 GTATTCTTGGCGTATCAATGGGATACCGCAGCAACACACACAAGTTCTCTTTATCGCCAA 1920
Qy      2054 AATCACGCCAAATAATAACGGGACCTATGCCTGTTTTGTCTCTAACTTGGCTACTGGCCG 2113
Db      1921 AATCACGCCAAATAATAACGGGACCTATGCCTGTTTTGTCTCTAACTTGGCTACTGGCCG 1980
Qy      2114 CAATAATTCCATAGTCAAGAGCATCACAGTCT---------------------------- 2145
Db      1981 CAATAATTCCATAGTCAAGAGCATCACAGTCTCTGCATCTGGAACTTCTCCTGGTCTCTC 2040
Qy      2146 ------------------------------------------------------------ 2145
Db      2041 AGCTGGGGCCACTGTCGGCATCATGATTGGAGTGCTGGTTGGGGTTGCTCTGATATAGCA 2100
Qy      2146 ------------------------------CTGACAGTTGTTTTGCTTCTTCCTTAAAG 2174
Db      2101 GCCCTGGTGTAGTTTCTTCATTTCAGGAAGACTGACAGTTGTTTTGCTTCTTCCTTAAAG 2160
Qy      2175 CATTTGCAACAGCTACAGTCTAAAATTGCTTCTTTACCAAGGATATTTACAGAAAAGACT 2234
Db      2161 CATTTGCAACAGCTACAGTCTAAAATTGCTTCTTTACCAAGGATATTTACAGAAAAGACT 2220
Qy      2235 CTGACCAGAGATCGAGACCATCCTAGCCAACATCGTGAAACCCCATCTCTACTAAAAATA 2294
Db      2221 CTGACCAGAGATCGAGACCATCCTAGCCAACATCGTGAAACCCCATCTCTACTAAAAATA 2280
Qy      2295 CAAAAATGAGCTGGGCTTGGTGGCGCGCACCTGTAGTCCCAGTTACTCGGGAGGCTGAGG 2354
Db      2281 CAAAAATGAGCTGGGCTTGGTGGCGCGCACCTGTAGTCCCAGTTACTCGGGAGGCTGAGG 2340
Qy      2355 CAGGAGAATCGCTTGAACCCGGGAGGTGGAGATTGCAGTGAGCCCAGATCGCACCACTGC 2414
Db      2341 CAGGAGAATCGCTTGAACCCGGGAGGTGGAGATTGCAGTGAGCCCAGATCGCACCACTGC 2400
Qy      2415 ACTCCAGTCTGGCAACAGAGCAAGACTCCATCTCAAAAAGAAAAGAAAAGAAGACTCTGA 2474
Db      2401 ACTCCAGTCTGGCAACAGAGCAAGACTCCATCTCAAAAAGAAAAGAAAAGAAGACTCTGA 2460
Qy      2475 CCTGTACTCTTGAATACAAGTTTCTGATACCACTGCACTGTCTGAGAATTTCCAAAACTT 2534
Db      2461 CCTGTACTCTTGAATACAAGTTTCTGATACCACTGCACTGTCTGAGAATTTCCAAAACTT 2520
```

```
Qy      2535 TAATGAACTAACTGACAGCTTCATGAAACTGTCCACCAAGATCAAGCAGAGAAAATAATT 2594
Db      2521 TAATGAACTAACTGACAGCTTCATGAAACTGTCCACCAAGATCAAGCAGAGAAAATAATT 2580
Qy      2595 AATTTCATGGGACTAAATGAACTAATGAGGATAATATTTTCATAATTTTTTATTTGAAAT 2654
Db      2581 AATTTCATGGGACTAAATGAACTAATGAGGATAATATTTTCATAATTTTTTATTTGAAAT 2640
Qy      2655 TTTGCTGATTCTTTAAATGTCTTGTTTCCCAGATTTCAGGAAACTTTTTTTCTTTTAAGC 2714
Db      2641 TTTGCTGATTCTTTAAATGTCTTGTTTCCCAGATTTCAGGAAACTTTTTTTCTTTTAAGC 2700
Qy      2715 TATCCACAGCTTACAGCAATTTGATAAAATATACTTTTGTGAACAAAAATTGAGACATTT 2774
Db      2701 TATCCACAGCTTACAGCAATTTGATAAAATATACTTTTGTGAACAAAAATTGAGACATTT 2760
Qy      2775 ACATTTTCTCCCTATGTGGTCGCTCCAGACTTGGGAAACTATTCATGAATATTTATATTG 2834
Db      2761 ACATTTTCTCCCTATGTGGTCGCTCCAGACTTGGGAAACTATTCATGAATATTTATATTG 2820
Qy      2835 TATGGTAATATAGTTATTGCACAAGTTCAATAAAAATCTGCTCTTTGTATGACAGAATAC 2894
Db      2821 TATGGTAATATAGTTATTGCACAAGTTCAATAAAAATCTGCTCTTTGTATGACAGAATAC 2880
Qy      2895 ATTTGAAAACATTGGTTATATTACCAAGACTTTGACTAGAATGTCGTAT 2943
Db      2881 ATTTGAAAACATTGGTTATATTACCAAGACTTTGACTAGAATGTCGTAT 2929
```

```
RESULT 4
E01630
LOCUS       E01630                  2928 bp    RNA     linear   PAT 29-SEP-1997
DEFINITION  cDNA encoding human carcinoembryonic antigen.
ACCESSION   E01630
VERSION     E01630.1  GI:2169883
KEYWORDS    JP 1988177794-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2928)
  AUTHORS   Oikawa,S. and Nakazato,H.
  TITLE     HUMAN CARCINOEMBRYONIC ANTIGEN ;
  JOURNAL   Patent: JP 1988177794-A 1 21-JUL-1988;
            SUNTORY LTD
COMMENT     OS   Human
            PN   JP 1988177794-A/1
            PD   21-JUL-1988
            PF   14-JAN-1987 JP 1987006851
            PI   OIKAWA SHINZO, NAKAZATO HIROSHI
            PC
            C12N15/00,C07H21/04,C07K13/00,C12P21/02,G01N33/574//G01N33/577, PC
             (C12P21/02,
            PC   C12R1:19);
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
            CC   *source: tissue_type=Colon tumor;
            CC   *source: clone=pCEA 80-11;
            FH   Key             Location/Qualifiers
            FH
            FT   mRNA            1. .2929
            FT   CDS             1. .2097
            FT                   /product='human carcinoembryonic antigen' FT
            sig_peptide     1. .60
            FT                   /product='signal peptide of human  FT
                 cacinoembryonic antigen'
            FT   mat_peptide     61. .2094
            FT                   /product='mature peptide of human  FT
                 carcinoembryonic antigen'
```